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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/724,915	11/28/2000	Naoki Nakayama	99,569-A	8656

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EXAMINER

ROMEO, DAVID S

ART UNIT	PAPER NUMBER
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1647

DATE MAILED: 03/19/2003

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

09/724,915

Applicant(s)

NAKAYAMA ET AL.

Examiner

David S Romeo

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 19 December 2002.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-56 is/are pending in the application.
- 4a) Of the above claim(s) 9,12-44 and 46-56 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-8,10,11 and 45 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☒ Claim(s) 1-56 are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
- Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
- 11) ☐ The proposed drawing correction filed on _____ is: a) ☐ approved b) ☐ disapproved by the Examiner.
- If approved, corrected drawings are required in reply to this Office action.
- 12) ☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

- 13) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- * See the attached detailed Office action for a list of the certified copies not received.
- 14) ☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).
- a) ☐ The translation of the foreign language provisional application has been received.
- 15) ☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) 5, 6.
- 4) ☐ Interview Summary (PTO-413) Paper No(s) _____.
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☐ Other:

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DETAILED ACTION

Claims 1-56 are pending.

Applicant's election with traverse of group I, claims 1-8, 10, 11, 45, and the species SEQ ID NO: 7 in Paper No. 11 is acknowledged. The traversal is on the ground(s) that it would not be an undue hardship to search SEQ ID NO: 7 and SEQ ID NO: 11. This is not found persuasive because an application may properly be required to be restricted to one of two or more claimed invention if they are able to support separate patents and they are either independent (MPEP § 806.04 - § 806.04 (j)) or distinct (MPEP § 806.05 - § 806.05(i)). SEQ ID NO: 7 and SEQ ID NO: 11 are distinct for the reasons given in the Office action mailed July 2, 2002 (Paper No. 9). Furthermore, SEQ ID NO: 7 and SEQ ID NO: 11, in spite of their similarity, are structurally distinct molecules and require separate searches of the literature and sequence databases and would therefore present an undue search burden. Furthermore, for each SEQ ID NO: there are three independent claims. For each independent claim there are at least 5, 6, and 8 Markush members. Therefore, for each SEQ ID NO: there are at least $5 \times 6 \times 8 = 240$ considerations. To examine SEQ ID NO: 7 and 11 together is to increase this burden two-fold.

The requirement is still deemed proper and is therefore made FINAL.

Claims 9, 12-44, 46-56 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in Paper No. 11.

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It is noted that in the restriction mailed July 2, 2002 (Paper No. 9), Applicants were notified that the restriction between the four sequences is not a requirement for an election of species but is rather a further requirement for restriction among independent and distinct inventions, and Applicants were required to elect one from A-D. In response Applicants elected

5 SEQ ID NO: 7. Insofar as SEQ ID NO: 7 encodes SEQ ID NO: 8, Applicants' election of SEQ ID NO: 7 has been construed as a constructive election of C, nucleic acid molecules encoding the polypeptide of SEQ ID NO: 8. Claims 1-8, 10, 11, 45 are being examined only to the extent that they read upon nucleic acid molecules encoding the polypeptide of SEQ ID NO: 8.

10 Applicant's election of the species BLASTN in Paper No. 14 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

Claim 11 is withdrawn from further consideration pursuant to 37 CFR 1.142(b) to the

15 extent that it is drawn to a nonelected species, there being no allowable generic or linking claim. Election was made **without** traverse in Paper No. 14.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

20 The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

25 The following is a quotation of the second paragraph of 35 U.S.C. 112:

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The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

5 Claims 1, 2, 4-8, 10, 11, 45 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

 The specification lacks complete deposit information for the deposit of the ATCC
10 Deposit No. that corresponds to SEQ ID NO: . While the specification provides enough information for one of skill in the art to produce a polynucleotide comprising a coding sequence with the same or similar properties as, reproduction of an identical polynucleotide is a highly unpredictable event. Because it does not appear that the ATCC Deposit No. that corresponds to SEQ ID NO: 7 is known and publicly available or can be reproducibly isolated from nature
15 without undue experimentation and because the claims require the use of the ATCC Deposit No. that corresponds to SEQ ID NO: 7, a suitable deposit of the clones is required for patent purposes.

 Applicants referral to the deposit of the ATCC Deposit No. that corresponds to SEQ ID NO: 7 at page 92 is insufficient to ensure that all of the conditions of 37 CFR § 1.801-1.809 have
20 been met.

 If the deposit was made under the provision of the Budapest Treaty, filing of an affidavit or declaration by applicants or assignees, or a statement by an attorney of record over his or her signature and registration number, stating that the deposit has been accepted by an International Depository Authority under the provisions of the Budapest Treaty, that all restrictions upon
25 public access to the deposit will be irrevocably removed upon the grant of a patent on this

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application and that the deposit will be replaced if viable samples cannot be dispensed by the depository, is required. This requirement is necessary when a deposit is made under the provisions of the Budapest Treaty as the treaty leaves these specific matters to the discretion of each State. Amendment of the specification to recite the date of the deposit and the complete
5 name and address of the depository, and amendment of the claims to refer to the accession number, is required. In addition, claims reciting the deposited material must be amended to include the depository accession number of the deposited material.

Furthermore, unless the deposit was made at or before the time of filing, a declaration under 37 CFR 1.132 is necessary to construct a chain of custody. The declaration, executed by a
10 person in a position to know, should identify the deposited clones by its depository accession number, establish that the deposited clones are the same as that described in the specification and establish that the deposited clone was in applicants' possession at the time of filing.

The new address for the ATCC, effective March 23, 1998, is American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209.

15
Claims 1-8, 10, 11, 45 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The present specification discloses polynucleotides
20 encoding the amino acid sequence of SEQ ID NO: 8 and exemplifies such a polynucleotide with SEQ ID NO: 7. The claims are directed to or encompass nucleic acid molecules that hybridize to the complement of such polynucleotides, or to polynucleotide variants of such polynucleotides,

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or to polynucleotides encoding variants of SEQ ID NO: 8; nucleic acid molecules encoding a polypeptide having a percent identity to the amino acid sequence of SEQ ID NO: 8; nucleic acid molecules comprising allelic or splice variants of polynucleotides encoding SEQ ID NO: 8, or other variants of polynucleotides encoding variants of SEQ ID NO: 8; nucleic acid molecules comprising fragments of polynucleotides encoding fragments of SEQ ID NO: 8; nucleic acid molecules encoding conservatively or non-conservatively amino acid substituted, inserted, or deleted variants of SEQ ID NO: 8. This rejection is meant to encompass any and/or all embodiments of the claims other than a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 7 or the nucleotide sequence of the insert of the deposited clone that corresponds to SEQ ID NO: 7, or a nucleic acid molecule encoding the amino acid sequence of SEQ ID NO: 8 or the amino acid sequence encoded by the deposited clone that corresponds to SEQ ID NO: 7.

In some instances the claims require that the polypeptide encoded by the claimed nucleic acid molecule possess an activity that is possessed by the polypeptide of SEQ ID NO: 8 or possess antigenic properties. However, the claims do not require that the polypeptide possess any particular biological activity, nor any particular conserved structure, or other disclosed distinguishing feature. Simply describing a large genus of any and/or all potential activities, as in, "an activity that is possessed by the polypeptide of SEQ ID NO: 8", is not sufficient to satisfy the written description requirement as to a particular biological activity. Nor does such a description lead those skilled in the art to a particular activity. The property of being "antigenic" says nothing regarding the particular antigenicity of the polypeptide or fragment. Thus, the claims are drawn to a genus of nucleic acid molecules encoding a genus of variant polypeptides

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that is specifically defined only by some level of nucleotide or amino acid sequence similarity.

The specification and claim do not indicate what distinguishing attributes shared by the members of the genus. In some cases, the specification and claim do not place any limit on the number of amino acid substitutions, deletions, insertions and/or additions that may be made to SEQ ID NO:

- 5 8. In some cases, the specification and claim do not place any limit on the number of nucleotide substitutions, deletions, insertions and/or additions that may be made to SEQ ID NO: 7 or to polynucleotides encoding SEQ ID NO: 8. The specification and claim do not provide any guidance as to what changes should be made. Structural features that could distinguish compounds in the genus from others in the protein class are missing from the disclosure. No
- 10 common structural attributes identify the members of the genus. The general knowledge and level of skill in the art do not supplement the omitted description because specific, not general, guidance is what is needed. Since the disclosure fails to describe the common attributes or characteristics that identify members of the genus and because the genus is highly variant, SEQ ID NO: 7 and polynucleotides encoding SEQ ID NO: 8, alone, are insufficient to describe the
- 15 genus. One of skill in the art would reasonably conclude that the disclosure fails to provide a representative number of species to describe the genus. Thus, applicant was not in possession of the claimed genus.

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus.

- 20 The factors to be considered include disclosure of complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, the only factor present in the claim

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is a partial structure in the form of some level of amino acid or nucleotide sequence identity.

There is not even identification of any particular portion of the structure that must be conserved.

Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus. Applicant

5 must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the written

description inquiry, whatever is now claimed. The specification does not clearly allow persons

of ordinary skill in the art to recognize that Applicants invented what is claimed. The skilled

artisan cannot envision the detailed chemical structure of the encompassed genus of

10 polynucleotides and/or polypeptides, and therefore conception is not achieved until reduction to

practice has occurred, regardless of the complexity or simplicity of the method of making or

isolation. Adequate written description requires more than a mere statement that it is part of the

invention and reference to a potential method of isolating or making it. The compound itself is

required. One cannot describe what one has not conceived. Therefore, only nucleic acid

15 molecules comprising the nucleotide sequence of SEQ ID NO: 7 or nucleic acid molecules

encoding the amino acid sequence of SEQ ID NO: 8, but not the full breadth of the claim meets

the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that

the written description provision of 35 U.S.C. §112 is severable from its enablement provision.

20 Claims 1-8, 10, 11, 45 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled

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in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The claims are directed to or encompass nucleic acid molecules that hybridize to the complement of such polynucleotides, or to polynucleotide variants of such polynucleotides, or to polynucleotides encoding variants of SEQ ID NO: 8; nucleic acid molecules encoding a polypeptide having a percent identity to the amino acid sequence of SEQ ID NO: 8; nucleic acid molecules comprising allelic or splice variants of polynucleotides encoding SEQ ID NO: 8, or other variants of polynucleotides encoding variants of SEQ ID NO: 8; nucleic acid molecules comprising fragments of polynucleotides encoding fragments of SEQ ID NO: 8; nucleic acid molecules encoding conservatively or non-conservatively amino acid substituted, inserted, or deleted variants of SEQ ID NO: 8. This rejection is meant to encompass any and/or all embodiments of the claims other than a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 7 or the nucleotide sequence of the insert of the deposited clone that corresponds to SEQ ID NO: 7, or a nucleic acid molecule encoding the amino acid sequence of SEQ ID NO: 8 or the amino acid sequence encoded by the deposited clone that corresponds to SEQ ID NO: 7. In some instances the claims require that the polypeptide encoded by the claimed nucleic acid molecule possess an activity that is possessed by the polypeptide of SEQ ID NO: 8 or possess antigenic properties. However, the claims do not require that the polypeptide possess any particular biological activity, nor any particular conserved structure, or other disclosed distinguishing feature. Simply describing a large genus of any and/or all potential activities, as in, "an activity that is possessed by the polypeptide of SEQ ID NO: 8", is not sufficient to describe a particular biological activity. Nor does such a description lead those

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skilled in the art to a particular activity. The property of being "antigenic" says nothing regarding the particular antigenicity of the polypeptide or fragment. Furthermore, there are no working examples of such variant polynucleotides and polypeptides possessing any and/or all activities encompassed by "an activity". The specification lacks guidance for the amino acids in

5 SEQ ID NO: 2 that are essential for "an activity" and structural integrity and those amino acids that are either expendable or substitutable. The skilled artisan is left to extensive experimentation wherein such variant polynucleotides and polypeptides are randomly made and through trial and error experimentation is left to determine how such variants can be used. Moreover, there is a lack of predictability in the art. Predicting structure, hence function, from

10 primary amino acid sequence data is extremely complex and there doesn't exist an efficient algorithm for predicting the structure of a given protein from its amino acid sequence alone. See Bowie (w8) page 1306, column 1, full paragraph 1, or Ngo (x8) page 433, full paragraph 1, and page 492, full paragraph 2.

In view of the breadth of the claims, the limited amount of direction and working

15 examples provided by the inventor, the unpredictability in the art and the quantity of experimentation needed to make or use the invention based on the content of the disclosure, it would require undue experimentation for the skilled artisan to make and/or use the full scope of the claimed invention.

20 The following claims are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

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Claims 1-8, 10, 11, 45 are indefinite over the recitation of "moderately or highly stringent conditions" because stringency varies according to the hybridization conditions and the particular hybrid under study. The specification fails to precisely define "moderately or highly stringent conditions". One of ordinary skill in the art would not be reasonably apprised of the metes and
5 bounds of the invention. The metes and bounds are not clearly set forth.

Claims 8, 10 are indefinite because they recite the term "CHL polypeptide". Because the instant specification does not identify that material element or combination of elements which is unique to, and, therefore, definitive of "CHL polypeptide" an artisan cannot determine what additional or material limitations are placed upon a claim by the presence of this element. The
10 metes and bounds are not clearly set forth.

Claims 2-8, 10, 11, 45 are indefinite over the recitation of "an activity" of the polypeptide set forth in SEQ ID NO: 8. Because the instant specification does not identify that material element or combination of elements which is unique to, and, therefore, definitive of "an activity" an artisan cannot determine what additional or material limitations are placed upon a claim by
15 the presence of this element. The metes and bounds are not clearly set forth. It is unclear what activity is intended.

Claims 1-8, 10, 11, 45 are indefinite over the recitation of "complementary to" because it is unclear if a nucleotide sequence that is a full length complement or a nucleotide sequence that is only complementary to some portion of a nucleic acid molecule is intended. The metes and
20 bounds are not clearly set forth.

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Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-4, 11 are rejected under 35 U.S.C. 102(a) as being anticipated by IMAGE clone 1857913, as evidenced by NCI-CGAP (u13) and The I.M.A.G.E. Consortium (v13).

NCI-CGAP (u13) discloses that IMAGE clone 1857913 is an isolated nucleic acid molecule comprising a nucleotide sequence that is 99.7% identical to nucleotides 734 - 1088 of the present application's SEQ ID NO: 7, as indicated below:

```

AI246227/c
LOCUS      AI246227          355 bp    mRNA    linear    EST 28-JAN-1999
DEFINITION qi29f01.x1 Soares_NhMPu_S1 Homo sapiens cDNA clone IMAGE:1857913
            3', mRNA sequence.
20 ACCESSION  AI246227
VERSION     AI246227.1  GI:3841624
KEYWORDS    EST.
SOURCE      human.
            ORGANISM  Homo sapiens
25            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 355)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
30 TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            JOURNAL    Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
35            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 710 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 263.
40 FEATURES  Location/Qualifiers
            source      1..355
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:1857913"
45                        /clone_lib="Soares_NhMPu_S1"
                        /tissue_type="Pooled human melanocyte, fetal heart, and
                        pregnant uterus"
                        /lab_host="DH10B"
                        /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                        (Pharmacia) with a modified polylinker; Site_1: Not I;

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Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

10 BASE COUNT 80 a 83 c 94 g 98 t
ORIGIN

15 Query Match 23.6%; Score 353.4; DB 9; Length 355;
Best Local Similarity 99.7%; Pred. No. 1.5e-86;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

20 Qy 734 ccaccgctctcactatgatccctccaccaagccgacaggtctgtcccgctttcc 793
Db 355 CCACCGCTCTCACTATGATCCTCCACCAAGCCGACAGGCTGGAGGTCTGTCCCGCTTTCC 296

25 Qy 794 tggggccagaagtcaccggggagctcttattggattcccagcaagcatcaggaaccattgt.853
Db 295 TGGGGCCAGAAGTCACCGGGGAGCTCTTATGGATTCCCAGCAAGCATCAGGAACCATTTGT 236

30 Qy 854 gcaaattgtcatcaataacaaacacaagcatggacaagtgtgtgtttccaatggaaagac 913
Db 235 GCAAATTGTCTATCAATAACAAACACAAGCATGGACAAGTGTGTGTTTCCAATGGAAAGAC 176

35 Qy 974 gctatgtacttghtaatgtcaccaagcaagagtgtgaagaaatccactgccccaatcgata 1033
Db 115 GCTATGTACTTGTAAATGTACCAAGCAAGAGTGTGAAGAAATCCACTGCCCCAATCGATA 56

40 Qy 1034 cccctgcaagtatcctcaaaaaatagacggaaagtgtgcaaggtgtgtccaggt 1088
Db 55 CCCCTGCAAGTATCCTCAAAAAATAGACGGAATGTGCAAGGTGTGTCCAGGT 1

Insofar as the isolated nucleic acid molecule was cloned then IMAGE clone 1857913

comprises the complement of the isolated nucleic acid molecule. The I.M.A.G.E. Consortium

(v13) indicates that IMAGE clone 1857913 was available to the public on 12/14/98 (page 13).

The nucleotide sequence that is 99.7% identical to nucleotides 734 - 1088 of the present

45 application's SEQ ID NO: 7, or the complement thereof, hybridizes as set forth in 1(d), 2(e), or 3(g), in the absence of evidence to the contrary. The metes and bounds of "complementary" are not clearly set forth. The nucleotide sequence that is 99.7% identical to nucleotides 734 - 1088 of the present application's SEQ ID NO: 7, or the complement thereof, is "complementary" as set forth in 1(e), 2(f), or 3 (h). The nucleotide sequence that is 99.7% identical to nucleotides

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734 - 1088 of the present application's SEQ ID NO: 7, or the complement thereof, comprises a region of the nucleotide sequence of SEQ ID NO: 7 or the ATCC Deposit No. that corresponds to SEQ ID NO: 7 that encodes a polypeptide fragment of at least about 25 amino acid residues, as indicated below:

```

5  alignment_scores:
      Quality: 118.00      Length: 118
      Ratio: 1.000      Gaps: 0
      Percent Similarity: 100.000      Percent Identity: 100.000

10 alignment_block:
    US-09-724-915-8 x AI246227/rev

15 Align seg 1/1 to reverse of: AI246227 from: 1 to: 355

202 HisArgSerHisTyrAspProProSerArgGlnAlaGlyGlyLeuSe 218
354 CACCGCTCTCACTATGATCCTCCACCAAGCCGACAGGCTGGAGGTCTGTC 305

218 rArgPheProGlyAlaArgSerHisArgGlyAlaLeuMetAspSerGlnG 235
304 CCGCTTTCTGGGGCCAGAAGTCACCGGGGAGCTCTTATGGATTCCCAGC 255

235 lnAlaSerGlyThrIleValGlnIleValIleAsnAsnLysHisLysHis 251
254 AAGCATCAGGAACCATTTGTGCAAATTGTTCATCAATAACAAACACAAGCAT 205

252 GlyGlnValCysValSerAsnGlyLysThrTyrSerHisGlyGluSerTr 268
204 GGACAAGTGTGTGTTTCCAATGGAAAGACCTATTCTCATGGCGAGTCCTG 155

268 pHisProAsnLeuArgAlaPheGlyIleValGluCysValLeuCysThrc 285
154 GCACCCAAACCTCCGGGCATTGGCATTGTGGAGTGTGCTATGTACTT 105

285 ysAsnValThrLysGlnGluCysLysLysIleHisCysProAsnArgTyr 301
104 GTAATGTCACCAAGCAAGAGTGTAAGAAAATCCACTGCCCAATCGATAC 55

302 ProCysLysTyrProGlnLysIleAspGlyLysCysCysLysValCysPr 318
54 CCTGCAAGTATCCTCAAAAAATAGACGGAAAAATGCTGCAAGGTGTGTCC 5

318 oGly 319
4 AGGT 1.

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The metes and bounds of "an activity of the encoded polypeptide" are not clearly set forth. The polypeptide fragment has an activity of the encoded polypeptide set forth in SEQ ID NO: 8 or is antigenic, in the absence of evidence to the contrary. The nucleotide sequence that is 99.7% identical to nucleotides 734 - 1088 of the present application's SEQ ID NO: 7 comprises a region, as set forth in 2(d), or a nucleotide sequence comprising a fragment, as set forth in 3(f), as indicated above. The nucleotide sequence that is 99.7% identical to nucleotides 734 - 1088 of the present application's SEQ ID NO: 7 comprises a nucleotide sequence encoding a polypeptide as set forth in 3(c), 3(d) or 3(e). The metes and bounds of "an activity of the encoded

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polypeptide” are not clearly set forth. The polypeptide fragment has an activity of the encoded polypeptide set forth in SEQ ID NO: 8, in the absence of evidence to the contrary.

The ability to determine percent identity by a given computer program or algorithm is viewed as a product-by-process limitation. The recitation of a process limitation is not viewed as positively limiting the claimed product absent a showing that the process imparts a novel property to the claimed product, as it is assumed that equivalent products are obtainable by multiple computer programs. The metes and bounds of “an activity of the encoded polypeptide” are not clearly set forth. The polypeptide or fragment thereof has an activity of the encoded polypeptide set forth in SEQ ID NO: 8 or is antigenic, in the absence of evidence to the contrary.

Claims 1-5, 7, 11 are rejected under 35 U.S.C. 102(a) as being anticipated by NCI-CGAP (u13).

The disclosure of NCI-CGAP (u13) discussed above is incorporated herein by reference. The structural and/or functional limitations of the nucleotide sequence that is 99.7% identical to nucleotides 734 - 1088 of the present application’s SEQ ID NO: 7 as discussed above is incorporated herein by reference. NCI-CGAP (u13) discloses the vector pT7T3D-Pac comprising IMAGE clone 1857913 and the prokaryotic host cell DH10B comprising the vector.

Claims 1-5, 7, 11, 45 are rejected under 35 U.S.C. 102(a) as being anticipated by Jacobs (10, cited by Applicants). Jacobs discloses an isolated nucleic acid molecule (SEQ ID NO: 75) 99.7% identical to nucleotides 44-1495 of the present application’s SEQ ID NO: 7, which

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encodes a polypeptide (SEQ ID NO: 76) 99.8% identical to the present application's SEQ ID

NO: 8, as indicated below:

AAZ33353
 ID AAZ33353 standard; cDNA; 3861 BP.
 XX
 AC AAZ33353;
 XX
 DT 29-FEB-2000 (first entry)
 XX
 DE Human secreted protein clone dw665_4 nucleotide sequence SEQ ID NO:75.
 XX
 KW Human; secreted protein; nutritional; cytokine; cell proliferation;
 KW differentiation; immune stimulating; vaccine; suppression;
 KW haematopoiesis regulation; tissue growth; activin; inhibin;
 KW chemotactic; chemokinetic; haemostatic; thrombolytic; receptor;
 KW ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
 KW tumour inhibition; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9957132-A1.
 XX
 PD 11-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-US09970.
 XX
 PR 07-MAY-1998; 98US-0084564.
 PR 02-JUN-1998; 98US-0087645.
 PR 22-JUL-1998; 98US-0093712.
 PR 31-JUL-1998; 98US-0094935.
 PR 10-AUG-1998; 98US-0095880.
 PR 11-AUG-1998; 98US-0096068.
 PR 06-MAY-1999; 99US-0096068.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Bowman MR;
 PI DiBlasio-Smith E, Widom A;
 XX
 DR WPI; 2000-052937/04.
 DR P-PSDB; AAY53035.
 XX
 PT New polynucleotides encoding secreted human proteins, derived from
 PT adult placenta, adult retina, fetal brain, fetal -
 XX
 PS Claim 84; Page 429-430; 492pp; English.
 XX
 CC The present invention describes new human secreted proteins which were
 CC isolated from adult placenta, adult retina, foetal brain, foetal kidney,
 CC adult blood, adult brain, adult thyroid, adult bladder, adult neural
 CC tissue, adult testes, and adult lymph node cDNA libraries. The human
 CC secreted proteins, and the polynucleotides encoding them, are predicted
 CC to have biological activities which would make them suitable for
 CC treating, preventing or ameliorating medical conditions in humans and
 CC animals. Suggested activities include nutritional activity, cytokine
 CC and cell proliferation/differentiation activity, immune stimulating
 CC (e.g. as vaccines) or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC cadherin/tumour invasion suppressor activity, and tumour inhibition
 CC activity. The polynucleotides are also stated to be useful for gene
 CC therapy. AAZ33316 to AAZ33373 encode human secreted proteins, and
 CC AAY52998 to AAY53060 represent human secreted proteins, given in the
 CC present invention.
 XX
 SQ Sequence 3861 BP; 1158 A; 797 C; 853 G; 1053 T; 0 other;

Query Match 95.9%; Score 1434.4; DB 21; Length 3861;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1448; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 44 gtgcacgcgtggcagacggagaaggccagtgcccagcttgagggttctgtccacotttttgc 103
 Db 1 gtgcacgcgtggcagacggagaaggccagtgcccagcttgagggttctgtccacotttttgc 60

Qy 104 agtgggtccaaatgagaaaaaagtggaaaatggaggagcatgaaatacatcttttcgttgtt 163
 Db 61 agtgggtccaaatgagaaaaaagtggaaaatggaggagcatgaaatacatcttttcgttgtt 120

Qy 164 gttctttcttttgcctagaaggaggcaaaacagagcaagtaaaacatttcagagacatttg 223

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5 Db 121 gttctttcttttcttagaaggaggcaaaacagagcaagtaaaacattcagagacatattg 180
Qy 224 catgtttcaagacaagaagtacagagtggtgagagatggcatccttacctggaacctta 283
Db 181 catgtttcaagacaagaagtacagagtggtgagagatggcatccttacctggaacctta 240
10 Qy 284 tgggttggtttactgcgtgaactgcattctgctcagagaatgggaatgtgctttgcagcgg 343
Db 241 tgggttggtttactgcgtgaactgcattctgctcagagaatgggaatgtgctttgcagcgg 300
Qy 344 agtcagatgtccaaatgttcattgcctttctcctgtgcatttcctcatctgtgtgccc 403
Db 301 agtcagatgtccaaatgttcattgcctttctcctgtgcatttcctcatctgtgtgccc 360
15 Qy 404 tcgctgcccaagaagactccttacccccagtgaaacaataaggtgaccagcaagctttgcga 463
Db 361 tcgctgccc--agactccttacccccagtgaaacaataaggtgaccagcaagctttgcga 417
20 Qy 464 gtacaattgggacaacttaccaacatggagagctgttcgtagctgaagggtctttcagaa 523
Db 418 gtacaattgggacaacttaccaacatggagagctgttcgtagctgaagggtctttcagaa 477
Qy 524 tcggcaacccaatcaatgcacccagtgagctgttcggagggaacgtgtattgtgtgtct 583
25 Db 478 tcggcaacccaatcaatgcacccagtgagctgttcggagggaacgtgtattgtgtgtct 537
Qy 584 caagaacttgcccaaatatacctgtgccttcccagtcctctgttcagattcctgtgtgccc 643
30 Db 538 caagaacttgcccaaatatacctgtgccttcccagtcctctgttcagattcctgtgtgccc 597
Qy 644 ggatgcagaggagatgggagaactgtcatgggaacattctgatggtgatattctccggca 703
Db 598 ggatgcagaggagatgggagaactgtcatgggaacattctgatggtgatattctccggca 657
35 Qy 704 acctgccacaagagaagcaagacattcttaccacccgctctcactatgatcctccaccaag 763
Db 658 acctgccacaagagaagcaagacattcttaccacccgctctcactatgatcctccaccaag 717
40 Qy 764 ccgacaggctggaggctgtgtcccgcttctcctggggccagaagtcacccgggagcttctat 823
Db 718 ccgacaggctggaggctgtgtcccgcttctcctggggccagaagtcacccgggagcttctat 777
45 Qy 824 ggattcccagcaagcatcaggaaccattgtgcaaatgtcatcaatacaaacacaagca 883
Db 778 ggattcccagcaagcatcaggaaccattgtgcaaatgtcatcaatacaaacacaagca 837
Qy 884 tggacaagtgtgtgtttccaatggaaagacctattctcatggcgagtcctggcaccacaaa 943
50 Db 838 tggacaagtgtgtgtttccaatggaaagacctattctcatggcgagtcctggcaccacaaa 897
Qy 944 cctccgggcatattggcattgtggagtgtgtgctatgtacttgaatgtcaccaagcaaga 1003
Db 898 cctccgggcatattggcattgtggagtgtgtgctatgtacttgaatgtcaccaagcaaga 957
55 Qy 1004 gtgtaagaaaaatccactgccccaatcgataccctcgcaagtatcctcaaaaaatagacgg 1063
Db 958 gtgtaagaaaaatccactgccccaatcgataccctcgcaagtatcctcaaaaaatagacgg 1017
60 Qy 1064 aaagtgtcgaagggtgtgtccaggtaaaaaagcaaaagaagaacttcaggccaaagctt 1123
Db 1018 aaagtgtcgaagggtgtgtccaggtaaaaaagcaaaagaagaacttcaggccaaagctt 1077
65 Qy 1124 tgacaataaaggctacttctcgggggaagaaacgatgcctgtgtatgagtcgtattcat 1183
Db 1078 tgacaataaaggctacttctcgggggaagaaacgatgcctgtgtatgagtcgtattcat 1137
70 Qy 1184 ggaggatggggagacaaccagaaaaatagcactgggagactgagagaccctcaggtaga 1243
Db 1138 ggaggatggggagacaaccagaaaaatagcactgggagactgagagaccctcaggtaga 1197
Qy 1244 ggtccacgcttggactattcgaaagggcattctccagcacttccatattgagaagatctc 1303
75 Db 1198 ggtccacgcttggactattcgaaagggcattctccagcacttccatattgagaagatctc 1257
Qy 1304 caagaggatgtttgaggagcttctcacttcaagctggtgaccagaaacacctgagcca 1363
Db 1258 caagaggatgtttgaggagcttctcacttcaagctggtgaccagaaacacctgagcca 1317
80 Qy 1364 gtggaagatcttcaaccgaaggagaagctcagatcagccagatgtgttcaagtcgtgtatg 1423
Db 1318 gtggaagatcttcaaccgaaggagaagctcagatcagccagatgtgttcaagtcgtgtatg 1377
85 Qy 1424 cagaacagagcttgaagatttagtcaaggttttgcacctggagagatctgaaaagggcca 1483
Db 1378 cagaacagagcttgaagatttagtcaaggttttgcacctggagagatctgaaaagggcca 1437
90 Qy 1484 ctgttaggcaag 1495
Db 1438 ctgttaggcaag 1449

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AAY53035

ID AAY53035 standard; Protein; 457 AA.

XX

AC AAY53035;

XX

DT 29-FEB-2000 (first entry)

XX

DE Human secreted protein clone dw665_4 protein sequence SEQ ID NO:76.

XX

KW Human; secreted protein; nutritional; cytokine; cell proliferation;
differentiation; immune stimulating; vaccine; suppression;
haematopoiesis regulation; tissue growth; activin; inhibin;
chemotactic; chemokinetic; haemostatic; thrombolytic; receptor;
ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
tumour inhibition; gene therapy.

XX

OS Homo sapiens.

XX

PN WO9957132-A1.

XX

PD 11-NOV-1999.

XX

PF 07-MAY-1999; 99WO-US09970.

XX

PR 07-MAY-1998; 98US-0084564.

PR 02-JUN-1998; 98US-0087645.

PR 22-JUL-1998; 98US-0093712.

PR 31-JUL-1998; 98US-0094935.

PR 10-AUG-1998; 98US-0095880.

PR 11-AUG-1998; 98US-0096068.

PR 06-MAY-1999; 99US-0096068.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Bowman MR;

PI DiBlasio-Smith E, Widom A;

XX

DR WPI; 2000-052937/04.

DR N-PSDB; AAZ33353.

XX

PT New polynucleotides encoding secreted human proteins, derived from
adult placenta, adult retina, fetal brain, fetal

XX

PS Claim 65; Page 430-432; 492pp; English.

XX

CC The present invention describes new human secreted proteins which were
isolated from adult placenta, adult retina, foetal brain, foetal kidney,
adult blood, adult brain, adult thyroid, adult bladder, adult neural
tissue, adult testes, and adult lymph node cDNA libraries. The human
secreted proteins, and the polynucleotides encoding them, are predicted
to have biological activities which would make them suitable for
treating, preventing or ameliorating medical conditions in humans and
animals. Suggested activities include nutritional activity, cytokine
and cell proliferation/differentiation activity, immune stimulating
(e.g. as vaccines) or suppressing activity, haematopoiesis regulating
activity, tissue growth activity, activin/inhibin activity,
chemotactic/chemokinetic activity, haemostatic and thrombolytic
activity, receptor/ligand activity, anti-inflammatory activity,
cadherin/tumour invasion suppressor activity, and tumour inhibition
activity. The polynucleotides are also stated to be useful for gene
therapy. AAZ33316 to AAZ33373 encode human secreted proteins, and
AAY52998 to AAY53060 represent human secreted proteins, given in the
present invention.

XX

SQ Sequence 457 AA;

Query Match 99.4%; Score 2520.5; DB 21; Length 457;

Best Local Similarity 99.8%; Pred. No. 3.1e-184;

Matches 451; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGGMKYIFSLFFLLLEGGKTEQVKHSETYCMFQDKKYRVGERWHPYLEPYGLVYCVNCI 60

Db 7 mggmkylfslffllleggkteqvkhssetycmfqdkkyrvgerwhpylepyglvycvnci 66

QY 61 CSENGNVLCSRVCPNVHCLSPVHIPLHCCPRCPEDSLPPVNNKVTSKSCEYNGTTYQH 120

Db 67 csengnvlcsrvcpnvhclspvhiplhccprcp-dslppvnnkvtsksceyngttyqh 125

QY 121 ELFVAEGLFQNRQPNQCTQCSCSEGNVYCGLKTCPKLTCAFPVSVSPDSCCRVCRGDGELS 180

Db 126 elfvaeqlfqnrdpnqctqcscsegnvygltcpkltcafpvsvpsccrvcrgdgels 185

QY 181 WEHSDGDIRQPANREARHSYHRSHYDPPPSRQAGGLSRFPGARSHRGALMDSQQASGTI 240

Db 186 wehsdgdirqpanrearsyhrshydpppsrqagglrsfpgarshrgalmdsqasgti 245

QY 241 VQIVINKKHKGQCVSVNGKTYSHGESWHPNLRFAFGIVECVLCTQNVTKQECKKIHCNPR 300

Db 241 vqivinkkhkgqcvsvngktyshgeswhpnlrfafgivecvlctqnvtkqeckkihcpnr 300

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Db 246 vqivinnkhkhgqvcvengktyshgeswhpnlrafgivecvlctenvtkqeckkihcpnr 305
QY 301 YPCKYPQKIDGKCKKCPGKKAKEELPGQSFQDNGYFCGEETMPVYESVFMEDGETTRKI 360
    |||
Db 306 ypckypqkidgkckkvcpgkkaakeelpgqsfdnkgycgeetmpvyesvfmmedgettrki 365
    |||
QY 361 ALETERRPPQVEVHVWTIRKGIHQHFHIEKISKRMFEELPHFKLVTRTTLSQWKIFTEGEA 420
    |||
Db 366 aleterppqvvehvwtirkgilqhfhiekiskrmfeelphfkltvtrttlsqwkiftegea 425
    |||
QY 421 QISQMCSSRVCRTLEDLVKVLYLERSEKQHC 452
    |||
Db 426 qismc SSRVCRTLEDLVKVLYLERSEKQHC 457.

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Jacobs also teaches polynucleotides encoding fragments of eight, i.e., "at least about 25",

2/23/13

or thirty amino acids, ~~amino acid~~ a polynucleotide which is an allelic variant, a polynucleotide that hybridizes under stringent conditions, polynucleotides linked to an expression control sequence, suitable host cells for the expression of the protein, transformed host cells, recombinant methods of producing the protein, viral vectors comprising the polynucleotides (page 118, line 6, through page 121, line 12; page 264, line 14, through page 267, line 2; page 292, line 8). The ability to determine percent identity by a given computer program or algorithm is viewed as a product-by-process limitation. The recitation of a process limitation is not viewed as positively limiting the claimed product absent a showing that the process imparts a novel property to the claimed product, as it is assumed that equivalent products are obtainable by multiple computer programs. The metes and bounds of "an activity of the encoded polypeptide" are not clearly set forth. The polypeptide or fragment thereof has an activity of the encoded polypeptide set forth in SEQ ID NO: 8 or is antigenic, in the absence of evidence to the contrary. The metes and bounds of "CHL polypeptide" are not clearly set forth. The polypeptide encoded by the isolated nucleic acid molecule is a "CHL polypeptide" in the absence of evidence to the contrary. The polypeptide has an additional six amino acids at the N-terminus. The isolated nucleic acid molecule encodes an allelic variant or splice variant of SEQ ID NO: 7 or the ATCC Deposit No. that corresponds to SEQ ID NO: 7. Jacob's isolated nucleic acid molecules and/or

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the complements thereof fall within the ambit of claims 1(d), 1(e), 2(a), 2(b), 2(c), 2(d), 2(e), 2(f), 3(a), 3(b), 3(c), 3(d), 3(e), 3(f), 3(g), 3(h).

Claims 3-8, 10, 45 are rejected under 35 U.S.C. 102(b) as being anticipated by Nathans

5 (a8). Embodiments 3(e), 3(f), 3(g), 3(h) of the present invention encompass essentially any and/or all nucleic acid molecules encoding any and/or all polypeptides. Nathans teaches an isolated nucleic acid molecule encoding a polypeptide, a viral vector comprising the nucleic acid molecule, eukaryotic and prokaryotic host cells comprising the vector, and methods of making the encoded polypeptide (Figure 1; column 6, last full paragraph; column 7, full paragraphs 1-3; 10 column 12, full paragraph 2).

Claims 1-8, 10, 45 are rejected under 35 U.S.C. 102(b) as being anticipated by Ruben (11, cited by Applicants). Ruben discloses a isolated nucleic acid molecule (SEQ ID NO: 47), or the complement thereof, that is 98.7% identical to the present application's SEQ ID NO: 7 and 15 that encodes amino acids 21-318 of the present application's SEQ ID NO: 8, as indicated below:

AAV34322/c
ID AAV34322 standard; DNA; 2315 BP.
XX
20 AC AAV34322;
XX
DT 29-JAN-1999 (first entry)
XX
DE Human secreted protein gene 20 clone HSDEG01.
XX
25 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
30 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
35 OS Homo sapiens.
XX
PN WO9840483-A2.
XX
PD 17-SEP-1998.
XX
40 PF 12-MAR-1998; 98WO-US04858.
XX
PR 19-DEC-1997; 97US-0068368.
PR 14-MAR-1997; 97US-0040710.
PR 14-MAR-1997; 97US-0040762.

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PR 30-MAY-1997; 97US-0048100.
PR 30-MAY-1997; 97US-0048189.
PR 30-MAY-1997; 97US-0048357.
PR 30-MAY-1997; 97US-0050934.
PR 06-JUN-1997; 97US-0048970.
PR 05-SEP-1997; 97US-0057765.

XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX
PI Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;
PI Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
PI Wei YF, Young PE, Zeng Z;

XX
DR WPI; 1998-520811/44.
DR P-PSDB; AAW75232.

XX
PT Isolated human poly:nucleotide(s) encoding secretory peptide(s) -
PT used to develop products for the diagnosis and treatment of e.g.
PT inflammation, cancers, CNS disorders or immune system disorders

XX
PS Claim 1; Page 148-149; 201pp; English.

XX
CC This sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number, and the clone it is derived
CC from, are detailed in the descriptor line. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV34277) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 28 novel genes and their fragments (nucleic
CC acid sequences: AAV34286-V34325; amino acid sequences AAW75196-W75235)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 28
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34286 for described uses).

XX
SQ Sequence 2315 BP; 582 A; 562 C; 510 G; 657 T; 4 other;

Query Match 86.0%; Score 1287; DB 19; Length 2315;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1312; Conservative 1; Mismatches 1; Indels 15; Gaps 1;

Qy 167 ctttcttttcttagaaggaggcaaaacagagcaagtaaaacattcagagacatattgcat 226
|||
Db 2107 CTTTCTTTTCTAGAGGAGGCMAAAACAGAGCAAGTAAACATTAGAGACATATTGCAT 2048
Qy 227 gtttcaagacaagaagtacagagtgggtgagagatggcatccttacctggaacottatgg 286
|||
Db 2047 GTTTCAGACAGAAAGTACAGAGTGAGGAGATGGCATCCTTACCTGGAACCTTATGG 1988
Qy 287 gttgggttactgcgtgaactgcattcgtcagagaaatgggaatgtgctttgagccaggt 346
|||
Db 1987 GTTGGTTTACTCGCTGAACATGCATCTGCTCAGAGAAATGGGAATGTGCTTTGAGCCGAGT 1928
Qy 347 cagatgtccaaatgttcattgcctttctcctgtgcatttcctcatctgtgctgcctcg 406
|||
Db 1927 CAGATGTCCAAATGTTTCATTGCTTTCTCTCTGTCATATTCCTCATCTGTGCTGCCCTCG 1868
Qy 407 ctgcccaagagactccttaccocagtgaaacaataaggtagaccagcaagtcttgcagta 466
|||
Db 1867 CTGCCCAGAGACTCCTTACCCCAAGTGAACAATAAGGTACCAGCAAGTCTTGCGAGTA 1808
Qy 467 caatggggacaacttaccaacatggagagctgttcgtagctgaagggtctttcagaatcg 526
|||
Db 1807 CAATGGGACAACCTTACCAACATGGAGAGCTGTTCTGAGCTGAAGGGCTCTTTCAGAAATCG 1748
Qy 527 gcaacccaatcaatgcacccagtgagctgttcggagggaacgtgtattgtggtctcaa 586
|||
Db 1747 GCAACCCAATCAATGCACCCAGTGAGCTGTTCTCGAGGGGAACGTGTATTGTGGTCTCAA 1688
Qy 587 gacttgcccaaatataacctgtgccttccagctctgttcagattcctgctgcgggt 646
|||
Db 1687 GACTTGCCCCAAATTAACCTGTGCCTTCCAGTCTCTGTTCCAGATTCTGTGCTGCCGGT 1628
Qy 647 atgcagaggagatggagaactgtcatgggaacattcgtatgggtgatattctccggcaacc 706
|||
Db 1627 ATGCAGAGGAGATGGAGAACTGTATGGGAACATCTGATGGTGATATCTTCCGGCAACC 1568
Qy 707 tgccaacagagagcaagacattcttaccacgctctcaactatgatcctccaccaagccg 766
|||
Db 1567 TGCCAACAGAGAGCAAGACATTCTTACCACCGCTCTCACTATGATCTCCACCAAGCCG 1508
Qy 767 acaggtgtgaggtctgtcccgctttcctggggcagaagtcacggggagctcttatgga 826
|||
Db 1507 ACAGGTGGAGGTCTGTCCCGCTTCTCGGGCCAGAAGTCACCGGGAGCTCTTATGGA 1448
Qy 827 ttccagcaagcatcaggaaccattgtgcaaatgtcatcaataacaaacacaagcatgg 886

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5 QY 887 acaagtgtgtgtttccaatggaaagacctattctcatggcgagtcctggcaccacaaacct 946
Db 1387 ACAAGTGTGTGTTTCCAATGGAAAGACCTATTCTCATGGCGAGTCCTGGCACCACAACT 1328

10 QY 947 cggggcatttggcattgtgagtggtgtgctatgtacttgaatgtcaccagcaagagtg 1006
Db 1327 CCGGGCATTTGCCATTGTGGAGTGTGTGCTATGTACTTGAATGTACCAAGCAAGAGTG 1268

15 QY 1007 taagaaaaatccactgccccaatcgataccccctgcaagtatcctcaaaaaatagacggaaa 1066
Db 1267 TAAGAAAAATCCACTGCCCCAATCGATACCCCTGCAAGTATCCTCAAAAAATAGACGGAAA 1208

20 QY 1067 gtgctgcaagggtgtgtccaggtaaaaaagcaaaagaagaacttccaggccaaagctttga 1126
Db 1207 ATGCTGCAAGGTGTGTCC-----AGAAGAACTTCCAGGCCAAAGCTTTGA 1163

25 QY 1127 caataaaggctacttctgcggggaagaaacgatgcctgtgatgagtggtattcatgga 1186
Db 1162 CAATAAAGGCTACTTCTGCGGGGAAGAAACGATGCCTGTGTATGAGTCTGTATTTCATGGA 1103

30 QY 1187 ggatggggagacaaccagaaaaatagcactggagactgagagaccacctcaggtagaggt 1246
Db 1102 GGATGGGGAGACAACAGAAAAATAGCACTGGAGACTGAGAGACCACCTCAGGTAGAGGT 1043

35 QY 1247 ccagtttggactattcgaaagggcattctccagcacttccatttgagaagatctccaa 1306
Db 1042 CCACGTTTGAGCTATTGAAAGGGCATTCTCCAGCACTTCATATTGAGAAGATCTCCAA 983

40 QY 1307 gaggatgttggaggagcttctcacttcaagctgggtgaccagaacaacccctgagccagtg 1366
Db 982 GAGGATGTTTGAGGAGCTTCTCACTTCAAGCTGGTGACCAGAACACCCTGAGCCAGTG 923

45 QY 1367 gaagatcttcacccaaggagaagctcagatcagccagatgtgttcaagtcgtgtatgcag 1426
Db 922 GAAGATCTTCACCGAAGGAGAAGCTCAGATCAGCCAGATGTGTTCAAGTCGTGTATGCAG 863

50 QY 1427 aacagagcttgaagatttagtcaaggttttgcacctggagagatctgaaaaggccactg 1486
Db 862 AACAGAGCTTGAAGATTTAGTCAAGGTTTGTACCTGGAGAGATCTGAAAAGGGCCACTG 803

55 QY 1487 ttaggcaag 1495
Db 802 TTAGGCAAG 794

60 ID AAV34322 standard; DNA; 2315 BP.
XX
AC AAV34322;
XX
DT 29-JAN-1999 (first entry)
XX

65 DE Human secreted protein gene 20 clone HSDEG01.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
60 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
65 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9840483-A2.
XX

70 PD 17-SEP-1998.
XX
PF 12-MAR-1998; 98WO-US04858.
XX

75 PR 19-DEC-1997; 97US-0068368.
PR 14-MAR-1997; 97US-0040710.
PR 14-MAR-1997; 97US-0040762.
PR 30-MAY-1997; 97US-0048100.
PR 30-MAY-1997; 97US-0048189.
80 PR 30-MAY-1997; 97US-0048357.
PR 30-MAY-1997; 97US-0050934.
PR 06-JUN-1997; 97US-0048970.
PR 05-SEP-1997; 97US-0057765.
XX

85 PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;
PI Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
PI Wei YF, Young PE, Zeng Z;
XX

90 DR WPI; 1998-520811/44.

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DR P-PSDB; AAW75232.

XX

PT Isolated human poly:nucleotide(s) encoding secretory peptide(s) -
PT used to develop products for the diagnosis and treatment of e.g.
PT inflammation, cancers, CNS disorders or immune system disorders

XX

PS Claim 1; Page 148-149; 201pp; English.

XX

CC This sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number, and the clone it is derived
CC from, are detailed in the descriptor line. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV34277) for increasing the stability of the fused
CC protein as compared to the human protein only.CC The invention relates to 28 novel genes and their fragments (nucleic
CC acid sequences: AAV34286-V34325; amino acid sequences AAW75196-W75235)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 28
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34286 for described uses).

XX

SQ Sequence 2315 BP; 582 A; 562 C; 510 G; 657 T; 4 other;

alignment_scores:

Quality:	298.00	Length:	298
Ratio:	1.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:

US-09-724-915-8 x AAV34322/rev

Align seg 1/1 to reverse of: AAV34322 from: 1 to: 2315

```
21 ThrGluGlnValLysHisSerGluThrTyrCysMetPheGlnAspLysLy 37
|||||
2082 ACAGAGCAAGTAAACATTTCAGAGACATATTGCATGTTTCAAGACAAGAA 2033

37 sTyrArgValGlyGluArgTrpHisProTyrLeuGluProTyrGlyLeuV 54
|||||
2032 GTACAGAGTGGGTGAGAGATGGCATCTTACCTGGAACCTTATGGGTGG 1983

54 alTyrCysValAsnCysIleCysSerGluAsnGlyAsnValLeuCysSer 70
|||||
1982 TTTACTGCGTGAAGTGCATCTGCTCAGAGAAATGGGAATGTGCTTTGCGAGC 1933

71 ArgValArgCysProAsnValHisCysLeuSerProValHisIleProHi 87
|||||
1932 CGAGTCAGATGTCCTAAATGTTTCATTGCTTTCTCTCTGTGCATATTCCTCA 1883

87 sLeuCysCysProArgCysProGluAspSerLeuProProValAsnAsnL 104
|||||
1882 TCTGTGCTGCCCTCGCTGCCGAGAGACTCCTTACCCCACTGAACAATA 1833

104 ysValThrSerLysSerCysGluTyrAsnGlyThrThrTyrGlnHisGly 120
|||||
1832 AGGTGACCAAGCAAGTCTTGGAGTACAAATGGGACAACTTACCAACATGGA 1783

121 GluLeuPheValAlaGluGlyLeuPheGlnAsnArgGlnProAsnGlnCy 137
|||||
1782 GAGCTGTTCTAGCTGAAGGCTCTTTTCAATCGGCAACCAATCAATG 1733

137 sThrGlnCysSerCysSerGluGlyAsnValTyrCysGlyLeuLysThrC 154
|||||
1732 CACCCAGTGCAGCTGTTCTGGAGGAAACGTGTATTGTGCTCAGAGCTT 1683

154 ysProLysLeuThrCysAlaPheProValSerValProAspSerCysCys 170
|||||
1682 GCCCAAAATTAACCTGTGCTTCCAGTCTCTGTTCCAGATTCTGTGCTGC 1633

171 ArgValCysArgGlyAspGlyGluLeuSerTrpGluHisSerAspGlyAs 187
|||||
1632 CGGTATGCAGAGGAGATGGAGAACTGTCTATGGGAACATTCTGATGTTGA 1583

187 pIlePheArgGlnProAlaAsnArgGluAlaArgHisSerTyrHisArgS 204
|||||
1582 TATCTTCCGGCAACCTGCCAACAGAGAGCAAGACATTCTTACCACCGCT 1533

204 erHisTyrAspProProProSerArgGlnAlaGlyGlyLeuSerArgPhe 220
|||||
1532 CTCATATGATCTCCACCAAGCCGACAGGCTGGAGGTCTGTCCCGCTTT 1483

221 ProGlyAlaArgSerHisArgGlyAlaLeuMetAspSerGlnGlnAlaSe 237
|||||
1482 CCTGGGGCCAGAGTCAACGGGGAGCTCTTATGATTTCCAGCAAGCATC 1433

237 rGlyThrIleValGlnIleValIleAsnAsnLysHisLysHisGlyGlnV 254
```


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|||||
1432 AGGAACCATTTGTGCAATTTGTCATCAATAACAAACACAGCATGGACAAG 1383
5 254 a lCysValSerAsnGlyLysThrTyrSerHisGlyGluSerTrpHisPro 270
|||||
1382 TGTGTGTTTCCAATGGAAAGACCTATTCTCATGGCGAGTCTGGCACCCA 1333
10 271 AsnLeuArgAlaPheGlyIleValGluCysValLeuCysThrCysAsnVa 287
|||||
1332 AACCTCCGGGCATTGTCATTGTGGAGTGTGTGCTATGTACTTGTAAATGT 1283
15 287 lThrLysGlnGluCysLysLysIleHisCysProAsnArgTyrProCysL 304
|||||
1282 CACCAAGCAAGAGTGTAAAGAAAATCCACTGCCCAATCGATACCCCTGCA 1233
304 ysTyrProGlnLysIleAspGlyLysCysCysLysValCysPro 318
|||||
1232 AGTATCCTCAAAAAATAGACGGAAAATGCTGCAAGGTGTGTCCA 1189.

Ruben also discloses an isolated nucleic acid molecule (SEQ ID NO: 30), or the complement thereof, that is 98% identical to the present application's SEQ ID NO: 7 and that encodes amino acids 157-318 of the present application's SEQ ID NO: 8, as indicated below:

AAV34305
ID AAV34305 standard; DNA; 1732 BP.
XX
AC AAV34305;
XX
DT 29-JAN-1999 (first entry)
XX
DE Human secreted protein gene 20 clone HSDEG01.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
35 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
40 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9840483-A2.
XX
45 PD 17-SEP-1998.
XX
PF 12-MAR-1998; 98WO-US04858.
XX
50 PR 19-DEC-1997; 97US-0068368.
PR 14-MAR-1997; 97US-0040710.
PR 14-MAR-1997; 97US-0040762.
PR 30-MAY-1997; 97US-0048100.
PR 30-MAY-1997; 97US-0048189.
55 PR 30-MAY-1997; 97US-0048357.
PR 30-MAY-1997; 97US-0050934.
PR 06-JUN-1997; 97US-0048970.
PR 05-SEP-1997; 97US-0057765.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
60 PI Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;
PI Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
PI Wei YF, Young PE, Zeng Z;
XX
65 DR WPI; 1998-520811/44.
DR P-PSDB; AAW75215.
XX
70 PT Isolated human poly:nucleotide(s) encoding secretory peptide(s) -
PT used to develop products for the diagnosis and treatment of e.g.
PT inflammation, cancers, CNS disorders or immune system disorders
XX
PS Claim 1; Page 132-133; 201pp; English.
XX
75 CC This sequence represents a nucleic acid molecule which encodes a
secreted human protein. The gene number, and the clone it is derived
from, are detailed in the descriptor line. The gene can be used to
generate fusion proteins by linking to the gene to a human immunoglobulin
Fc portion (e.g. AAV34277) for increasing the stability of the fused

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CC protein as compared to the human protein only.
CC The invention relates to 28 novel genes and their fragments (nucleic
CC acid sequences: AAV34286-V34325; amino acid sequences AAW75196-W75235)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 28
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34286 for described uses).
XX
SQ Sequence 1732 BP; 507 A; 362 C; 418 G; 442 T; 3 other;

Query Match 60.0%; Score 897.2; DB 19; Length 1732;
Best Local Similarity 98.0%; Pred. No. 7.5e-270;
Matches 921; Conservative 3; Mismatches 1; Indels 15; Gaps 1;

QY 556 gttcggagggaacgtgtattgtggtctcaagacttgcgcccaataaacctgtgccttcc 615
Db 1 gttcggagggaacgtgtattgtggtctcaagmmttgcgcccaataaacctgtgccttcc 60

QY 616 cagtctctgttccagattcctgctgccgggtatgcagaggagatggagaactgtcatggg 675
Db 61 cagtctctgttccagattcctgctgccgggtatgcagaggagatggagaactgtcatggg 120

QY 676 aacattctgatggtgatattctccggcaacctgccacagagaagcaagacattcttacc 735
Db 121 aacattctgatggtgatattctccggcaacctgccacagagaagcaagacattcttacc 180

QY 736 accgctctcactatgatcctccaccaagccgacaggctggaggctctgtcccgctttcctg 795
Db 181 accgctctcactatgatcctccaccaagccgacaggctggaggctctgtcccgctttcctg 240

QY 796 gggccagaagtcacccgggagctcttatggattccacagcaagcatcaggaaccattgtgc 855
Db 241 gggccagaagtcacccgggagctcttatggattccacagcaagcatcaggaaccattgtgc 300

QY 856 aaattgtcatcaataaacaacaagcatggacaagtgtgtgtttccaatggaaagacct 915
Db 301 aaattgtcatcaataaacaacaagcatggacaagtgtgtgtttccaatggaaagacct 360

QY 916 attctcatggcagctcctggcaccacaaacctccgggcatttggcattgtggagtgtgtgc 975
Db 361 attctcatggcagctcctggcaccacaaacctccgggcatttggcattgtggagtgtgtgc 420

QY 976 tatgtacttgaatgtcaccaagcaagagtgtgaagaaatccactgccccaatcgatacc 1035
Db 421 tatgtacttgaatgtcaccaagcaagagtgtgaagaaatccactgccccaatcgatacc 480

QY 1036 cctgcaagtatccctcaaaaaatagacggaaagtgtgcaagggtgtgtccaggtaaaaaag 1095
Db 481 cctgcaagtatccctcaaaaaatagacggaaagtgtgcaagggtgtgtcc----- 529

QY 1096 caaaagaagaacttccaggccaaagctttgacaataaaggctacttctcggggaagaaa 1155
Db 530 ----agaagaacttccaggccaaagctttgacaataaaggctacttctcggggaagaaa 585

QY 1156 cgatgcctgtgtatgagtctgtattcatggaggatggggagacaaccagaaaaatagcac 1215
Db 586 cgatgcctgtgtatgagtctgtattcatggaggatggggagacaaccagaaaaatagcac 645

QY 1216 tggagactgagagaccacctcaggtagaggtccacgtttggactattcgaaagggcattc 1275
Db 646 tggagactgagagaccacctcaggtagaggtccacgtttggactattcgaaagggcattc 705

QY 1276 tccagcacttccatattgagaagatctccaagaggatgtttgaggagcttctcacttca 1335
Db 706 tccagcacttccatattgagaagatctccaagaggatgtttgaggagcttctcacttca 765

QY 1336 agctgggtgaccagaacaacctgagccagtggaagatcttccaggaaggagaagctcaga 1395
Db 766 agctgggtgaccagaacaacctgagccagtggaagatcttccaggaaggagaagctcaga 825

QY 1396 tcagccagatgtgttcaagtcgtgtatgcagaacagagcttgaagatttagtcaagggtt 1455
Db 826 tcagccagatgtgttcaagtcgtgtatgcagaacagagcttgaagatttagtcaagggtt 885

QY 1456 tgtacctggagagatctgaaaagggccactgttaggcaag 1495
Db 886 tgtacctggagagatctgaaaagggccactgttaggcaag 925

ID AAV34305 standard; DNA; 1732 BP.

XX

AC AAV34305;

XX

DT 29-JAN-1999 (first entry)

XX

DE Human secreted protein gene 20 clone HSDEG01.

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XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
5 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
10 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9840483-A2.
XX
15 PD 17-SEP-1998.
XX
PF 12-MAR-1998; 98WO-US04858.
XX
PR 19-DEC-1997; 97US-0068368.
20 PR 14-MAR-1997; 97US-0040710.
PR 14-MAR-1997; 97US-0040762.
PR 30-MAY-1997; 97US-0048100.
PR 30-MAY-1997; 97US-0048189.
25 PR 30-MAY-1997; 97US-0048357.
PR 30-MAY-1997; 97US-0050934.
PR 06-JUN-1997; 97US-0048970.
PR 05-SEP-1997; 97US-0057765.
XX
30 PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;
PI Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
PI Wei YF, Young PE, Zeng Z;
35 XX
DR WPI; 1998-520811/44.
DR P-PSDB; AAW75215.
XX
40 PT Isolated human poly:nucleotide(s) encoding secretory peptide(s) -
PT used to develop products for the diagnosis and treatment of e.g.
PT inflammation, cancers, CNS disorders or immune system disorders
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PS Claim 1; Page 132-133; 201pp; English.
XX
45 CC This sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number, and the clone it is derived
CC from, are detailed in the descriptor line. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV34277) for increasing the stability of the fused
50 CC protein as compared to the human protein only.
CC The invention relates to 28 novel genes and their fragments (nucleic
CC acid sequences: AAV34286-V34325; amino acid sequences AAW75196-W75235)
CC which are useful for preventing, treating or ameliorating medical
55 CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 28
CC polynucleotides, based on which tissues they are most highly expressed in
60 CC (see AAV34286 for described uses).
XX
SQ Sequence 1732 BP; 507 A; 362 C; 418 G; 442 T; 3 other;

alignment_scores:

65 Quality: 162.00 Length: 162
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

70 US-09-724-915-8 x AAV34305 ..

Align seg 1/1 to: AAV34305 from: 1 to: 1732

75 157 LeuThrCysAlaPheProValSerValProAspSerCysCysArgValCy 173
|||||
45 TTAACCTGTGCTCTCCAGTCTCTGTTCAGATTCTGCTGCCGGTATG 94
|||||
173 sArgGlyAspGlyGluLeuSerTrpGluHisSerAspGlyAspIlePheA 190
|||||
80 95 CAGAGGAGATGGAGAACTGTCATGGGAACATTCTGATGGTGATATCTTCC 144
|||||
190 rgGlnProAlaAsnArgGluAlaArgHisSerTyrHisArgSerHisTyr 206
|||||
145 GGCAACCTGCCAACAGAGCAAGACATTCTTACCACCGCTCTCACTAT 194
|||||
85 207 AspProProProSerArgGlnAlaGlyGlyLeuSerArgPheProGlyAl 223
|||||
195 GATCCTCCACCAAGCCGACAGGCTGGAGGTCTGTCCCGCTTTCCTGGGGC 244
|||||
90 223 aArgSerHisArgGlyAlaLeuMetAspSerGlnGlnAlaSerGlyThrI 240
|||||

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245 CAGAAGTCACCGGGGAGCTCTTATGGATTCCCAGCAAGCATCAGGAACCA 294
 240 leValGlnIleValIleAsnAsnLysHisLysHisGlyGlnValCysVal 256
 295 TTGTGCAAAATTGTCATCAATAACAAACAAGCATGGACAAGTGTGTGT 344
 257 SerAsnGlyLysThrTyrSerHisGlyGluSerTrpHisProAsnLeuAr 273
 345 TCCAATGGAAAGACCTATTCTCATGGCGAGTCCTGGCACCCAAACCTCCG 394
 273 gAlaPheGlyIleValGluCysValLeuCysThrCysAsnValThrLysG 290
 395 GGCATTGGCATTGTGGAGTGTGTCTATGTACTTGTAAATGTCACCAAGC 444
 290 InGluCysLysLysIleHisCysProAsnArgTyrProCysLysTyrPro 306
 445 AAGAGTGTAAAGAAAATCCACTGCCCAATCGATACCCCTGCAAGTATCCT 494
 307 GlnLysIleAspGlyLysCysCysLysValCysPro 318
 495 CAAAAAATAGACGAAAATGCTGCAAGGTGTGTCCA 530

Ruben also discloses allelic variants (paragraph bridging pages 41-42), N- and C-terminal truncations of the encoded polypeptide (page 42, last full paragraph), polynucleotide and polypeptide fragments (pages 44-45), vectors, host cells, and protein production (pages 48-49). Ruben's isolated nucleic acid molecules and/or the complements thereof fall within the ambit of claims 1(d), 1(e), 2(a), 2(b), 2(c), 2(d), 2(e), 2(f), 3(a), 3(b), 3(c), 3(d), 3(e), 3(f), 3(g), 3(h).

Conclusion

No claims are allowable. SEQ ID NO: 7 and a polynucleotide encoding the amino acid sequence of SEQ ID NO: 8 are free of the prior art of record.

ANY INQUIRY CONCERNING THIS COMMUNICATION OR EARLIER COMMUNICATIONS FROM THE EXAMINER SHOULD BE DIRECTED TO DAVID S. ROMEO WHOSE TELEPHONE NUMBER IS (703) 305-4050. THE EXAMINER CAN NORMALLY BE REACHED ON MONDAY THROUGH FRIDAY FROM 7:30 A.M. TO 4:00 P.M.

IF ATTEMPTS TO REACH THE EXAMINER BY TELEPHONE ARE UNSUCCESSFUL, THE EXAMINER'S SUPERVISOR, GARY KUNZ, CAN BE REACHED ON (703) 308-4623.

IF SUBMITTING OFFICIAL CORRESPONDENCE BY FAX, APPLICANTS ARE ENCOURAGED TO SUBMIT OFFICIAL CORRESPONDENCE TO THE FOLLOWING TC 1600 BEFORE AND AFTER FINAL RIGHTFAX NUMBERS:

BEFORE FINAL (703) 872-9306

AFTER FINAL (703) 872-9307

IN ADDITION TO THE OFFICIAL RIGHTFAX NUMBERS ABOVE, THE TC 1600 FAX CENTER HAS THE FOLLOWING OFFICIAL FAX NUMBERS: (703) 305-3592, (703) 308-4242 AND (703) 305-3014.

CUSTOMERS ARE ALSO ADVISED TO USE CERTIFICATE OF FACSIMILE PROCEDURES WHEN SUBMITTING A REPLY TO A NON-FINAL OR FINAL OFFICE ACTION BY FACSIMILE (SEE 37 CFR 1.6 AND 1.8).

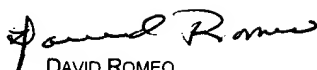
FAXED DRAFT OR INFORMAL COMMUNICATIONS SHOULD BE DIRECTED TO THE EXAMINER AT (703) 308-0294.

ANY INQUIRY OF A GENERAL NATURE OR RELATING TO THE STATUS OF THIS APPLICATION OR PROCEEDING SHOULD BE DIRECTED TO THE GROUP RECEPTIONIST WHOSE TELEPHONE NUMBER IS (703) 308-0196.

Application/Control Number: 09/724,915

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DAVID ROMEO
PRIMARY EXAMINER
ART UNIT 1647

5

DSR
MARCH 18, 2003